

SEQUENCE LISTING

<110> Lok, Si
 Conklin, Darrell C.
 Adams, Robyn L.
 Jelmsberg, Anna C.
 Lofton-Day, Catherine E.
 Jaspers, Stephen R.
 Stamm, Mike R.

<120> TESTIS-SPECIFIC INSULIN HOMOLOG POLYPEPTIDES

<130> 96-06C3

<150> 08/905,267

<151> 1997-08-01

<150> 60/023,213

<151> 1996-08-02

<150> 60/031,592

<151> 1996-11-21

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<211> 566

<212> DNA

<213> Rattus norvegicus

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1				5					10				15			

gct	cct	ttc	tcc	cag	gaa	caa	gaa	gag	gtc	acc	agc	ccc	acg	aag	ttg	96
Ala	Pro	Phe	Ser	Gln	Glu	Gln	Glu	Glu	Val	Thr	Ser	Pro	Thr	Lys	Leu	
			20					25					30			

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tgc ggc agg gac ctg ttg gta gaa gtt ata aaa ctc tgt ggc caa aat 144
 Cys Gly Arg Asp Leu Leu Val Glu Val Ile Lys Leu Cys Gly Gln Asn
 35 40 45

gac tgg agc cgg ttc tcg atg gaa gag caa agt cct atg aca gag ttg 192
 Asp Trp Ser Arg Phe Ser Met Glu Glu Gln Ser Pro Met Thr Glu Leu
 50 55 60

gtt ccc caa tat aca cgg aaa gtc aaa acc ttc aac cct cac cgg tcc 240
 Val Pro Gln Tyr Thr Arg Lys Val Lys Thr Phe Asn Pro His Arg Ser
 65 70 75 80

tcc tcc tcc tgg gga aga ttc aca aac cca ggc gtc tcc cag aag aaa 288
 Ser Ser Ser Trp Gly Arg Phe Thr Asn Pro Gly Val Ser Gln Lys Lys
 85 90 95

gca aca cac act tgg gaa tct cag tca ctg ccc aac tat cag ctt aaa 336
 Ala Thr His Thr Trp Glu Ser Gln Ser Leu Pro Asn Tyr Gln Leu Lys
 100 105 110

aag gag gag ctg ctt ccg aag aca gga gtg cat tca tac cac ggt ggc 384
 Lys Glu Glu Leu Leu Pro Lys Thr Gly Val His Ser Tyr His Gly Gly
 115 120 125

aag ccc tat gtg aag agt gta aaa ttt cag aag aaa aac act gac aaa 432
 Lys Pro Tyr Val Lys Ser Val Lys Phe Gln Lys Lys Asn Thr Asp Lys
 130 135 140

atg agt acc ttc agc ggc tta ttt tgg ggg aac cat ccc cag agg aag 480
 Met Ser Thr Phe Ser Gly Leu Phe Trp Gly Asn His Pro Gln Arg Lys
 145 150 155 160

cgc aga ggt ttc gca gat aaa tgc tgt gct ata ggg tgc tcc aaa gag 528
 Arg Arg Gly Phe Ala Asp Lys Cys Cys Ala Ile Gly Cys Ser Lys Glu
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gag ctg gcc gtc gca tgc ctt ccg ttt gtt gat ttt ta 566
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<213> Rattus norvegicus

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 35 40 45
 Asp Trp Ser Arg Phe Ser Met Glu Glu Gln Ser Pro Met Thr Glu Leu
 50 55 60
 Val Pro Gln Tyr Thr Arg Lys Val Lys Thr Phe Asn Pro His Arg Ser
 65 70 75 80
 Ser Ser Ser Trp Gly Arg Phe Thr Asn Pro Gly Val Ser Gln Lys Lys
 85 90 95
 Ala Thr His Thr Trp Glu Ser Gln Ser Leu Pro Asn Tyr Gln Leu Lys
 100 105 110
 Lys Glu Glu Leu Leu Pro Lys Thr Gly Val His Ser Tyr His Gly Gly
 115 120 125
 Lys Pro Tyr Val Lys Ser Val Lys Phe Gln Lys Lys Asn Thr Asp Lys
 130 135 140
 Met Ser Thr Phe Ser Gly Leu Phe Trp Gly Asn His Pro Gln Arg Lys
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taccagttcg	aaagcccgca	aaccgcttcc	ccggcccggg	gaagaggcac	aaacccagtg	300
tctacttctt	gggaagaagc	agtaaacagt	tgggaaatgc	agtcactacc	tgagtataag	360
gataaaaagg	gatattcacc	ccttggtctg	ctggagtttg	ctggaggccc	actccagatg	420
ctgtttgcct	gggtatcacc	agcagaggct	gcagaacagc	aaagattgct	gcctgttcct	480
tcctctggaa	gcttcattcc	agaggggcac	ccactagatg	ccagccagag	ctttcctgta	540
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gga ctc ctg ctg gtt cgg ttt tct cgt gaa ctg agc gac atc agc agt      100
Gly Leu Leu Leu Val Arg Phe Ser Arg Glu Leu Ser Asp Ile Ser Ser
              15              20              25

gcc agg aag ctg tgc ggc agg tac ttg gtg aaa gaa ata gaa aaa ctc      148
Ala Arg Lys Leu Cys Gly Arg Tyr Leu Val Lys Glu Ile Glu Lys Leu
              30              35              40

tgc ggc cat gcc aac tgg agc cag ttc cgt ttc gag gag gaa acc cct      196
Cys Gly His Ala Asn Trp Ser Gln Phe Arg Phe Glu Glu Glu Thr Pro
              45              50              55              60

ttc tca cgg ttg att gca cag gcc tcg gag aag gtc gaa gcc tac agc      244
Phe Ser Arg Leu Ile Ala Gln Ala Ser Glu Lys Val Glu Ala Tyr Ser
              65              70              75

cca tac cag ttc gaa agc ccg caa acc gct tcc ccg gcc cgg gga aga      292
Pro Tyr Gln Phe Glu Ser Pro Gln Thr Ala Ser Pro Ala Arg Gly Arg
              80              85              90

ggc aca aac cca gtg tct act tct tgg gaa gaa gca gta aac agt tgg      340
Gly Thr Asn Pro Val Ser Thr Ser Trp Glu Glu Ala Val Asn Ser Trp
              95              100              105

gaa atg cag tca cta cct gag tat aag gat aaa aag gga tat tca ccc      388
Glu Met Gln Ser Leu Pro Glu Tyr Lys Asp Lys Lys Gly Tyr Ser Pro
              110              115              120

ctt ggt aag aca aga gaa ttt tct tca tca cat aat atc aat gta tat      436
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Cys Gly Arg Tyr Leu Val Lys Glu Ile Glu Lys Leu Cys Gly His Ala
 35          40          45
Asn Trp Ser Gln Phe Arg Phe Glu Glu Glu Thr Pro Phe Ser Arg Leu
 50          55          60
Ile Ala Gln Ala Ser Glu Lys Val Glu Ala Tyr Ser Pro Tyr Gln Phe
 65          70          75          80
Glu Ser Pro Gln Thr Ala Ser Pro Ala Arg Gly Arg Gly Thr Asn Pro
 85          90          95
Val Ser Thr Ser Trp Glu Glu Ala Val Asn Ser Trp Glu Met Gln Ser
 100         105         110
Leu Pro Glu Tyr Lys Asp Lys Lys Gly Tyr Ser Pro Leu Gly Lys Thr

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115 120 125
 Arg Glu Phe Ser Ser Ser His Asn Ile Asn Val Tyr Ile His Glu Asn
 130 135 140
 Ala Lys Phe Gln Lys Lys Arg Arg Asn Lys Ile Lys Thr Leu Ser Asn
 145 150 155 160
 Leu Phe Trp Gly His His Pro Gln Arg Lys Arg Arg Gly Tyr Ser Glu
 165 170 175
 Lys Cys Cys Leu Thr Gly Cys Thr Lys Glu Glu Leu Ser Ile Ala Cys
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28

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